We claim:

1. A method for the production of ketocarotenoids by culturing genetically modified plants which show a modified ketolase activity in petals in comparison with the wild type.

2. The method according to claim 1 wherein plants are used whose petals already show a ketolase activity as the wild type and wherein the genetic modification brings about an increase of the ketolase activity in petals in comparison with the wild type.

3. The method according to claim 2, wherein, to increase the ketolase activity, the gene expression of a nucleic acid encoding a ketolase is increased in comparison with the wild type.

4. The method according to claim 3, wherein, to increase the gene expression, nucleic acids which encode ketolases are introduced into the plant.

5. The method according to claim 1, wherein plants are used whose petals show no ketolase activity as the wild type and wherein the genetic modification brings about a ketolase activity in petals in comparison with the wild type.

6. The method according to claim 5, wherein genetically modified plants are used which transgenically express a ketolase in petals.

7. The method according to claim 5 or 6, wherein, to bring about the gene expression, nucleic acids which encode ketolases are introduced into the plant.

8. The method according to claim 4 or 7, wherein nucleic acids are introduced which encode a protein comprising the amino acid sequence SEQ ID NO: 2 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 2 and which has the enzymatic characteristic of a ketolase.

Seq. + Fig.

9. The method according to claim 8, wherein nucleic acids comprising the sequence SEQ ID NO: 1 are introduced.

10. The method according to claim 4 or 7, wherein nucleic acids are introduced which encode a protein comprising the amino acid sequence SEQ ID NO: 16 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 16 and which has the enzymatic characteristic of a ketolase.

11. The method according to claim 10, wherein nucleic acids comprising the sequence SEQ ID NO: 15 are introduced.

12. The method according to any of claims 1 to 11, wherein genetically modified plants are used which show the highest expression rate of a ketolase in flowers.

13. The method according to claim 12, wherein the gene expression of the ketolase takes place under the control of a flower-specific promoter.

14. The method according to any of claims 1 to 13, wherein the plants additionally show an increased activity of at least one of the activities selected from the group consisting of hydroxylase activity and β-cyclase activity in comparison with the wild type.

15. The method according to claim 14, wherein, to additionally increase at least one of the activities, the gene expression of at least one nucleic acid selected from the group consisting of nucleic acids encoding a hydroxylase and nucleic acids encoding a β-cyclase is increased in comparison with the wild type.

16. The method according to claim 15, wherein, to increase the gene expression of at least one of the nucleic acids, at least one nucleic acid selected from the group consisting of nucleic acids encoding a hydroxylase and nucleic acids encoding a β-cyclase is introduced into the plant.

17. The method according to claim 16, wherein nucleic acids encoding a hydroxylase comprising the amino acid sequence SEQ ID NO: 18 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 20% identity at the amino acid level with the

sequence SEQ ID NO: 18 are introduced as nucleic acid encoding a hydroxylase.

18. The method according to claim 17, wherein nucleic acids comprising the sequence SEQ ID NO: 17 are introduced.

19. The method according to claim 16, wherein nucleic acids encoding a β-cyclase comprising the amino acid sequence SEQ ID NO: 20 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 20 are introduced as nucleic acid encoding a β-cyclase.

20. The method according to claim 19, wherein nucleic acids comprising the sequence SEQ ID NO: 19 are introduced.

21. The method according to any of claims 14 to 20, wherein genetically modified plants are used which have the highest expression rate of a hydroxylase and/or β-cyclase in flowers.

22. The method according to claim 21, wherein the gene expression of the hydroxylase and/or β-cyclase is effected under the control of a flower-specific promoter.

23. The method according to any of claims 1 to 22, wherein the plants additionally show a reduced ε-cyclase activity in comparison with the wild type.

24. The method according to claim 23, wherein the reduction of the ε-cyclase activity in plants is achieved by at least one of the following methods:

a) introducing, into plants, at least one double-stranded ε-cyclase ribonucleic acid sequence or (an) expression cassette(s) which ensure(s) its expression,
b) introducing, into plants, at least one ε-cyclase antisense ribonucleic acid sequence or an expression cassette which ensures its expression,
c) introducing, into plants, at least one ε-cyclase antisense ribonucleic acid sequence in combination with a ribozyme or (an) expression cassette(s) which ensure(s) its expression,
d) introducing, into plants, at least one ε-cyclase sense ribonucleic acid sequence for inducing a cosuppression or an expression cassette which ensures its expression,

e) introducing, into plants, at least one DNA- or protein-binding factor against an ε-cyclase gene, an ε-cyclase RNA or an ε-cyclase protein or an expression cassette which ensures its expression,

f) introducing, into plants, at least one viral nucleic acid sequence which brings about the degradation of ε-cyclase RNA or an expression cassette which ensures its expression,

g) introducing, into plants, at least one construct for generating an insertion, deletion, inversion or mutation in an ε-cyclase gene.

25. The method according to claim 24, embodiment a), wherein an RNA is introduced, into the plant, which has a region with double-stranded structure and comprises, in this region, a nucleic acid sequence which

a) is identical to at least a part of the plant's homologous ε-cyclase transcript and/or

b) is identical to at least a part of the plant's homologous ε-cyclase promoter sequence.

26. The method according to claim 25, wherein the region with double-stranded structure comprises a nucleic acid sequence which is identical to at least a part of the plant's homologous ε-cyclase transcript and which comprises the 5' terminus or the 3' terminus of the plant's homologous nucleic acid encoding an ε-cyclase.

27. The method according to claims 23 to 26, wherein genetically modified plants are used which show the lowest expression rate of an ε-cyclase in flowers.

28. The method according to claim 27, wherein the transcription of the double-stranded ε-cyclase ribonucleic acid sequence according to claim 24, embodiment a) and/or the antisense sequences according to claim 24, embodiment b), takes place under the control of a flower-specific promoter.

29. The method according to any of claims 5 to 28, wherein the plants show, in comparison with the wild type, additionally an increased activity of at least one of the activities selected from the group consisting of HMG-CoA reductase activity, (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase activity, 1-deoxy-D-xylose-5-phosphate synthase activity, 1-deoxy-D-xylose-5-phosphate reductoisomerase

activity, isopentenyl-diphosphate Δ-isomerase activity, geranyl-diphosphate synthase activity, farnesyl-diphosphate synthase activity, geranylgeranyl-diphosphate synthase activity, phytoene synthase activity, phytoene desaturase activity, zeta-carotene desaturase activity, crtISO activity, FtsZ activity and MinD activity.

30. The method according to claim 29, wherein, to additionally increase at least one of the activities, the gene expression of at least one nucleic acid selected from the group consisting of nucleic acids encoding an HMG-CoA reductase, nucleic acids encoding an (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase, nucleic acids encoding a 1-deoxy-D-xylose-5-phosphate synthase, nucleic acids encoding a 1-deoxy-D-xylose-5-phosphate reductoisomerase, nucleic acids encoding an isopentenyl-diphosphate Δ-isomerase, nucleic acids encoding a geranyl-diphosphate synthase, nucleic acids encoding a farnesyl-diphosphate synthase, nucleic acids encoding a geranylgeranyl-diphosphate synthase, nucleic acids encoding a phytoene synthase, nucleic acids encoding a phytoene desaturase, nucleic acids encoding a zeta-carotene desaturase, nucleic acids encoding a crtISO protein, nucleic acids encoding an FtsZ protein and nucleic acids encoding a MinD protein in comparison with the wild type.

31. The method according to claim 30, wherein, to increase the gene expression of at least one of the nucleic acids, at least one nucleic acid selected from the group consisting of nucleic acids encoding an HMG-CoA reductase, nucleic acids encoding an (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase, nucleic acids encoding a 1-deoxy-D-xylose-5-phosphate synthase, nucleic acids encoding a 1-deoxy-D-xylose-5-phosphate reductoisomerase, nucleic acids encoding an isopentenyl-diphosphate Δ-isomerase, nucleic acids encoding a geranyl-diphosphate synthase, nucleic acids encoding a farnesyl-diphosphate synthase, nucleic acids encoding a geranylgeranyl-diphosphate synthase, nucleic acids encoding a phytoene synthase, nucleic acids encoding a phytoene desaturase, nucleic acids encoding a zeta-carotene desaturase, nucleic acids encoding a crtISO protein, nucleic acids encoding an FtsZ protein and nucleic acids encoding a MinD protein are introduced into the plant.

32. The method according to claim 31, wherein nucleic acids encoding an HMG-CoA reductase comprising the amino acid sequence SEQ ID NO: 100 or a sequence derived from this

sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 100, are introduced as nucleic acid encoding an HMG-CoA reductase.

33. The method according to claim 32, wherein nucleic acids comprising the sequence SEQ ID NO: 99 are introduced.

34. The method according to claim 31, wherein nucleic acids encoding an (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase comprising the amino acid sequence SEQ ID NO: 102 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 102, are introduced as nucleic acid encoding an (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase.

35. The method according to claim 34, wherein nucleic acids comprising the sequence SEQ ID NO: 101 are introduced.

36. The method according to claim 31, wherein nucleic acids encoding a 1-deoxy-D-xylose-5-phosphate synthase comprising the amino acid sequence SEQ ID NO: 104 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 104, are introduced as nucleic acid encoding a 1-deoxy-D-xylose-5-phosphate synthase.

37. The method according to claim 36, wherein nucleic acids comprising the sequence SEQ ID NO: 103 are introduced.

38. The method according to claim 31, wherein nucleic acids encoding a 1-deoxy-D-xylose-5-phosphate reductoisomerase comprising the amino acid sequence SEQ ID NO: 106 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 106, are introduced as nucleic acid encoding a 1-deoxy-D-xylose-5-phosphate reductoisomerase.

39. The method according to claim 38, wherein nucleic acids comprising the sequence SEQ ID NO: 105 are introduced.

40. The method according to claim 31, wherein nucleic acids encoding an isopentenyl-diphosphate Δ-isomerase comprising the amino acid sequence SEQ ID NO: 108 or a sequence derived

from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 108, are introduced as nucleic acid encoding an isopentenyl-diphosphate Δ-isomerase.

41. The method according to claim 40, wherein nucleic acids comprising the sequence SEQ ID NO: 107 are introduced.

42. The method according to claim 31, wherein nucleic acids encoding a geranyl-diphosphate synthase comprising the amino acid sequence SEQ ID NO: 110 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 110, are introduced as nucleic acid encoding a geranyl-diphosphate synthase.

43. The method according to claim 42, wherein nucleic acids comprising the sequence SEQ ID NO: 106 are introduced.

44. The method according to claim 31, wherein nucleic acids encoding a farnesyl-diphosphate synthase comprising the amino acid sequence SEQ ID NO: 112 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 112, are introduced as nucleic acid encoding a farnesyl-diphosphate synthase.

45. The method according to claim 44, wherein nucleic acids comprising the sequence SEQ ID NO: 111 are introduced.

46. The method according to claim 31, wherein nucleic acids encoding a geranylgeranyl-diphosphate synthase comprising the amino acid sequence SEQ ID NO: 114 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 114, are introduced as nucleic acid encoding a geranylgeranyl-diphosphate synthase.

47. The method according to claim 46, wherein nucleic acids comprising the sequence SEQ ID NO: 113 are introduced.

48. The method according to claim 31, wherein nucleic acids encoding a phytoene synthase comprising the amino acid sequence SEQ ID NO: 116 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid

level with the sequence SEQ ID NO: 116, are introduced as nucleic acid encoding a phytoene synthase.

49. The method according to claim 48, wherein nucleic acids comprising the sequence SEQ ID NO: 115 are introduced.

50. The method according to claim 31, wherein nucleic acids encoding a phytoene desaturase comprising the amino acid sequence SEQ ID NO: 118 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 118, are introduced as nucleic acid encoding a phytoene desaturase.

51. The method according to claim 50, wherein nucleic acids comprising the sequence SEQ ID NO: 117 are introduced.

52. The method according to claim 31, wherein nucleic acids encoding a zeta-carotene desaturase comprising the amino acid sequence SEQ ID NO: 120 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 120, are introduced as nucleic acid encoding a zeta-carotene desaturase.

53. The method according to claim 52, wherein nucleic acids comprising the sequence SEQ ID NO: 119 are introduced.

54. The method according to claim 31, wherein nucleic acids encoding a crtISO protein comprising the amino acid sequence SEQ ID NO: 122 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 122, are introduced as nucleic acid encoding a crtISO protein.

55. The method according to claim 54, wherein nucleic acids comprising the sequence SEQ ID NO: 121 are introduced.

56. The method according to claim 31, wherein nucleic acids encoding an FtsZ protein comprising the amino acid sequence SEQ ID NO: 124 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 124, are introduced as nucleic acid encoding an FtsZ protein.

57. The method according to claim 56, wherein nucleic acids comprising the sequence SEQ ID NO: 123 are introduced.

58. The method according to claim 31, wherein nucleic acids encoding a MinD protein comprising the amino acid sequence SEQ ID NO: 126 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids, which has at least 20% identity at the amino acid level with the sequence SEQ ID NO: 126, are introduced as nucleic acid encoding a MinD protein.

59. The method according to claim 58, wherein nucleic acids comprising the sequence SEQ ID NO: 125 are introduced.

60. The method according to any of claims 29 to 59, wherein genetically modified plants are used which show the highest expression rate of an HMG-CoA reductase and/or (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase and/or 1-deoxy-D-xylose-5-phosphate synthase and/or 1-deoxy-D-xylose-5-phosphate reductoisomerase and/or isopentenyl-diphosphate Δ-isomerase and/or geranyl-diphosphate synthase and/or farnesyl-diphosphate synthase and/or geranylgeranyl-diphosphate synthase and/or phytoene synthase and/or phytoene desaturase and/or zeta-carotene desaturase and/or of a crtISO protein and/or of an FtsZ protein and/or of a MinD protein in flowers.

61. The method according to claim 60, wherein the gene expression of the HMG-CoA reductase and/or (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase and/or 1-deoxy-D-xylose-5-phosphate synthase and/or 1-deoxy-D-xylose-5-phosphate reductoisomerase and/or isopentenyl-diphosphate Δ-isomerase and/or geranyl-diphosphate synthase and/or farnesyl-diphosphate synthase and/or geranylgeranyl-diphosphate synthase and/or phytoene synthase and/or phytoene desaturase and/or zeta-carotene desaturase and/or of the crtISO protein and/or of the FtsZ protein and/or of the MinD protein takes place under the control of a flower-specific promoter.

62. The method according to any of claims 5 to 61, wherein the plants additionally show a reduced endogenous β-hydroxylase activity in comparison with the wild type.

63. The method according to claim 62, wherein reduction of the endogenous β-hydroxylase activity in plants is achieved by at least one of the following methods:

a) introducing, into plants, at least one double-standard endogenous β-hydroxylase ribonucleic acid sequence or (an) expression cassette(s) which ensure(s) its expression,

b) introducing, into plants, at least one endogenous β-hydroxylase antisense ribonucleic acid sequence or an expression cassette which ensures its expression,

c) introducing, into plants, at least one endogenous β-hydroxylase antisense ribonucleic acid sequence in combination with a ribozyme, or (an) expression cassette(s) which ensure(s) its expression,

d) introducing, into plants, at least one endogenous β-hydroxylase sense ribonucleic acid sequence for inducing a cosuppression or an expression cassette which ensures its expression,

e) introducing, into plants, at least one DNA- or protein-binding factor against an endogenous β-hydroxylase gene, β-hydroxylase RNA or β-hydroxylase protein or an expression cassette which ensures its expression,

f) introducing, into plants, at least one viral nucleic acid sequence which brings about the degradation of endogenous β-hydroxylase RNA or an expression cassette which ensures its expression,

g) inserting, into plants, at least one construct for generating an insertion, deletion, inversion or mutation in an endogenous β-hydroxylase gene.

64. The method according to claim 63, embodiment a), wherein an RNA is introduced, into the plant which has a region with double-stranded structure and comprises, in this region, a nucleic acid sequence which

a) is identical to at least a part of the plant's homologous, endogenous β-hydroxylase transcript and/or

b) is identical to at least a part of the plant's homologous, endogenous β-hydroxylase promoter sequence.

65. The method according to claim 64, wherein the region with double-stranded structure comprises a nucleic acid sequence which is identical to at least a part of the plant's homologous, endogenous β-hydroxylase transcript and which

comprises the 5' terminus or the 3' terminus of the plant's homologous nucleic acid encoding an endogenous β-hydroxylase.

66. The method according to claims 62 to 65, wherein genetically modified plants are used which show the lowest expression rate of an endogenous β-hydroxylase in flowers.

67. The method according to claim 66, wherein the transcription of the double-stranded endogenous β-hydroxylase ribonucleic acid sequence according to claim 63, embodiment a) and/or the antisense sequences according to claim 63, embodiment b), takes place under the control of a flower-specific promoter.

68. The method according to any of claims 5 to 67, wherein the plant used is a plant which has chromoplasts in petals.

69. The method according to any of claims 5 to 68, wherein the plant used is a plant selected from the families Ranunculaceae, Berberidaceae, Papaveraceae, Cannabaceae, Rosaceae, Fabaceae, Linaceae, Vitaceae, Brassiceae, Cucurbitaceae, Primulaceae, Caryophyllaceae, Amaranthaceae, Gentianaceae, Geraniaceae, Caprifoliaceae, Oleaceae, Tropaeolaceae, Solanaceae, Scrophulariaceae, Asteraceae, Liliaceae, Amaryllidaceae, Poaceae, Orchidaceae, Malvaceae, Illiaceae or Lamiaceae.

70. The method according to claim 65, wherein the plant used is a plant selected from the plant genera consisting of Marigold, Tagetes erecta, Tagetes patula, Acacia, Aconitum, Adonis, Arnica, Aqulegia, Aster, Astragalus, Bignonia, Calendula, Caltha, Campanula, Canna, Centaurea, Cheiranthus, Chrysanthemum, Citrus, Crepis, Crocus, Curcurbita, Cytisus, Delonia, Delphinium, Dianthus, Dimorphotheca, Doronicum, Eschscholtzia, Forsythia, Fremontia, Gazania, Gelsemium, Genista, Gentiana, Geranium, Gerbera, Geum, Grevillea, Helenium, Helianthus, Hepatica, Heracleum, Hisbiscus, Heliopsis, Hypericum, Hypochoeris, Impatiens, Iris, Jacaranda, Kerria, Laburnum, Lathyrus, Leontodon, Lilium, Linum, Lotus, Lycopersicon, Lysimachia, Maratia, Medicago, Mimulus, Narcissus, Oenothera, Osmanthus, Petunia, Photinia, Physalis, Phyteuma, Potentilla, Pyracantha, Ranunculus, Rhododendron, Rosa, Rudbeckia, Senecio, Silene, Silphium, Sinapsis, Sorbus, Spartium, Tecoma, Torenia, Tragopogon, Trollius, Tropaeolum, Tulipa, Tussilago, Ulex, Viola or Zinnia.

71. The method according to any of claims 1 to 70, wherein, after cultivation, the genetically modified plants are harvested and the ketocarotenoids are subsequently isolated from the plant's petals.

72. The method according to any of claims 1 to 71, wherein the ketocarotenoids are selected from the group consisting of astaxanthin, canthaxanthin, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, adonirubin und adonixanthin.

73. A nucleic acid construct comprising, in functional linkage, a flower-specific promoter and a nucleic acid encoding a ketolase.

74. A nucleic acid construct comprising, in functional linkage, a petal-specific promoter and a nucleic acid encoding a ketolase.

75. A nucleic acid construct comprising at least one nucleic acid encoding a ketolase and additionally at least one further nucleic acid selected from the group consisting of

a) nucleic acids encoding a β-cyclase,
b) nucleic acids encoding a β-hydroxylase,
c) nucleic acids encoding an HMG-CoA reductase,
d) nucleic acids encoding an (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase,
e) nucleic acids encoding a 1-deoxy-D-xylose-5-phosphate synthase,
f) nucleic acids encoding a 1-deoxy-D-xylose-5-phosphate reductoisomerase,
g) nucleic acids encoding an isopentenyl-diphosphate Δ-isomerase,
h) nucleic acids encoding a geranyl-diphosphate synthase,
i) nucleic acids encoding a farnesyl-diphosphate synthase,
j) nucleic acids encoding a geranylgeranyl-diphosphate synthase,
k) nucleic acids encoding a phytoene synthase,
l) nucleic acids encoding a phytoene desaturase,
m) nucleic acids encoding a zeta-carotene desaturase,
n) nucleic acids encoding a crtISO protein,
o) nucleic acids encoding an FtsZ protein,
p) nucleic acids encoding a MinD protein,
q) double-stranded endogenous β-hydroxylase ribonucleic acid sequence and/or endogenous β-hydroxylase antisense ribonucleic acid sequences and
r) double-stranded ε-cyclase ribonucleic acid sequence and/or ε-cyclase antisense ribonucleic acid sequence,

where the nucleic acids are functionally linked to one or more regulatory signals which ensure the transcription and translation in plants.

76. A double-stranded RNA molecule comprising

a) a sense RNA strand comprising at least one ribonucleotide sequence which is essentially identical to at least a part of the sense RNA ε-cyclase transcript, and

b) an antisense RNA strand which is essentially complementary to the RNA sense strand of a).

77. A double-stranded RNA molecule comprising

a) a sense RNA strand comprising at least one ribonucleotide sequence which is essentially identical to at least a part of the sense RNA transcript of the promoter region of an ε-cyclase gene, and

b) an antisense RNA strand which is essentially complementary to the RNA sense strand of a).

78. The double-stranded RNA molecule according to claim 76, where the cDNA sequence which can be derived from the ε-cyclase transcript is described by SEQ ID NO: 38.

79. The double-stranded RNA molecule according to claim 77, where the nucleic acid sequence of the promoter region of the ε-cyclase gene is described by SEQ ID NO: 47.

80. The double-stranded RNA molecule according to any of claims 76 to 79, where sense RNA strand and antisense RNA strand are bonded covalently with one another in the form of an inverted repeat.

81. A double-stranded RNA molecule comprising

a) a sense RNA strand comprising at least one ribonucleotide sequence which is essentially identical to at least a part of the sense RNA transcript of the endogenous β-hydroxylase, and

b) an antisense RNA strand which is essentially complementary to the RNA sense strand of a).

82. A double-stranded RNA molecule comprising

a) a sense RNA strand comprising at least one ribonucleotide sequence which is essentially identical to at least a part of the sense RNA transcript of the promoter region of the endogenous β-hydroxylase gene, and

b) an antisense RNA strand which is essentially complementary to the RNA sense strand of a).

83. The double-stranded RNA molecule according to claim 83, where the cDNA sequence which can be derived from the endogenous β-hydroxylase transcript is described by SEQ ID NO: 103.

84. A transgenic expression cassette comprising, in functional linkage with a promoter which is functional in plant organisms, a nucleic acid sequence transcribing a double-stranded RNA molecule according to any of claims 76 to 83.

85. The transgenic expression cassette according to claim 84, where the promoter is a flower-specific promoter.

86. A genetically modified plant, where the genetic modification

A in the event that the wild-type plant already shows ketolase activity in the petals, increases the activity of a ketolase in petals in comparison with the wild type, and

B in the event that the wild-type plant shows no ketolase activity in petals, produces the activity of a ketolase in petals in comparison with the wild type.

87. The genetically modified plant according to claim 86, wherein the increase or production of the ketolase activity is brought about by an increase or production of the gene expression of a nucleic acid encoding a ketolase in comparison with the wild type.

88. The genetically modified plant according to claim 87, wherein, to increase or produce the gene expression, nucleic acids which encode ketolases are introduced into the plant.

89. A genetically modified plant which has chromoplasts in the petals, wherein the genetically modified plant comprises at least one transgenic nucleic acid encoding a ketolase.

90. The genetically modified plant according to any of claims 86 to 89, wherein the genetic modification additionally increases, in comparison with a wild-type plant, at least one of the activities selected from the group consisting of hydroxylase activity and β-cyclase activity.

91. The genetically modified plant according to any of claims 86 to 90, wherein the genetic modification additionally reduces the ε-cyclase activity in comparison with a wild-type plant.

92. The genetically modified plant according to any of claims 86 to 91, wherein the genetic modification additionally increases, in comparison with a wild-type plant, at least one of the activities selected from the group consisting of HMG-CoA reductase activity, (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate reductase activity, 1-deoxy-D-xylose-5-phosphate synthase activity, 1-deoxy-D-xylose-5-phosphate reductoisomerase activity, isopentenyl-diphosphate Δ-isomerase activity, geranyl-diphosphate synthase activity, farnesyl-diphosphate synthase activity, geranylgeranyl-diphosphate synthase activity, phytoene synthase activity, phytoene desaturase activity, zeta-carotene desaturase activity, crtISO activity, FtsZ activity and MinD activity.

93. The genetically modified plant according to any of claims 86 to 92, wherein, the genetic modification additionally reduces the endogenous β-hydroxylase activity in comparison with a wild-type plant.

94. The genetically modified plant according to any of claims 86 to 93, wherein the plant is selected from the plant families Ranunculaceae, Berberidaceae, Papaveraceae, Cannabaceae, Rosaceae, Fabaceae, Linaceae, Vitaceae, Brassiceae, Cucurbitaceae, Primulaceae, Caryophyllaceae, Amaranthaceae, Gentianaceae, Geraniaceae, Caprifoliaceae, Oleaceae, Tropaeolaceae, Solanaceae, Scrophulariaceae, Asteraceae, Liliaceae, Amaryllidaceae, Poaceae, Orchidaceae, Malvaceae, Illiaceae or Lamiaceae.

95. The genetically modified plant according to claim 94, selected from the group consisting of the plant genera Marigold, Tagetes erecta, Tagetes patula, Lycopersicon, Rosa,

Calendula, Physalis, Medicago, Helianthus, Chrysanthemum, Aster, Tulipa, Narcissus, Petunia, Geranium, or Tropaeolum or Adonis.

96. The genetically modified plant according to any of claims 86 to 95, wherein the ketolase is expressed in petals.

97. The genetically modified plant according to any of claims 86 to 96, wherein the expression rate of a ketolase is highest in petals.

98. The use of the genetically modified plants according to any of claims 86 to 97 as ornamentals or as feeds and foods.

99. The use of the petals of the genetically modified plants according to any of claims 86 to 97 for the production of ketocarotenoid-comprising extracts or for the production of feed additives and food additives.

100. A method for the generation of genetically modified plants according to claim 97, wherein a nucleic acid construct comprising, in functional linkage, a flower-specific promoter and nucleic acids encoding a ketolase is introduced into the genome of the starting plant.